

Fig. 2

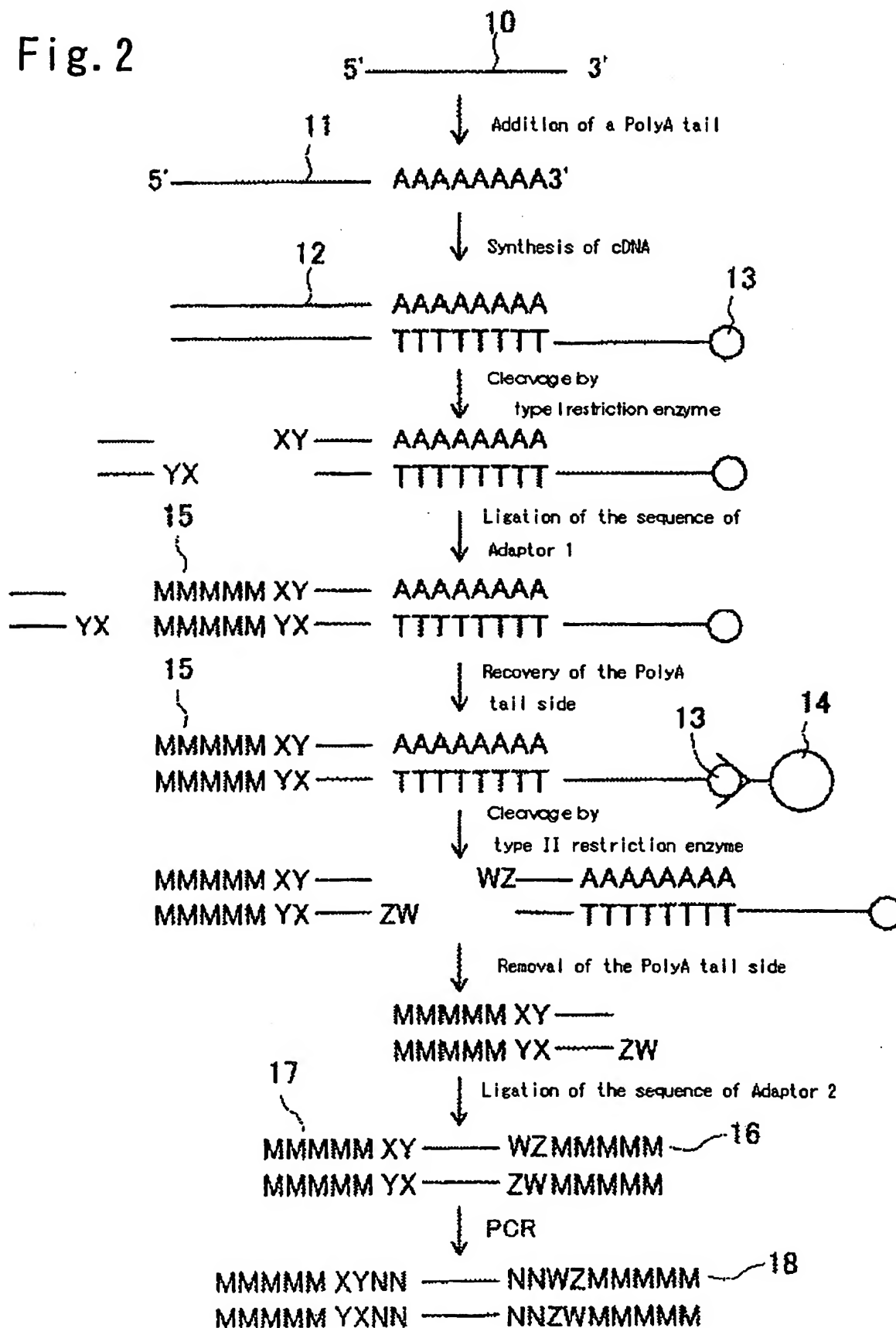


Fig. 3

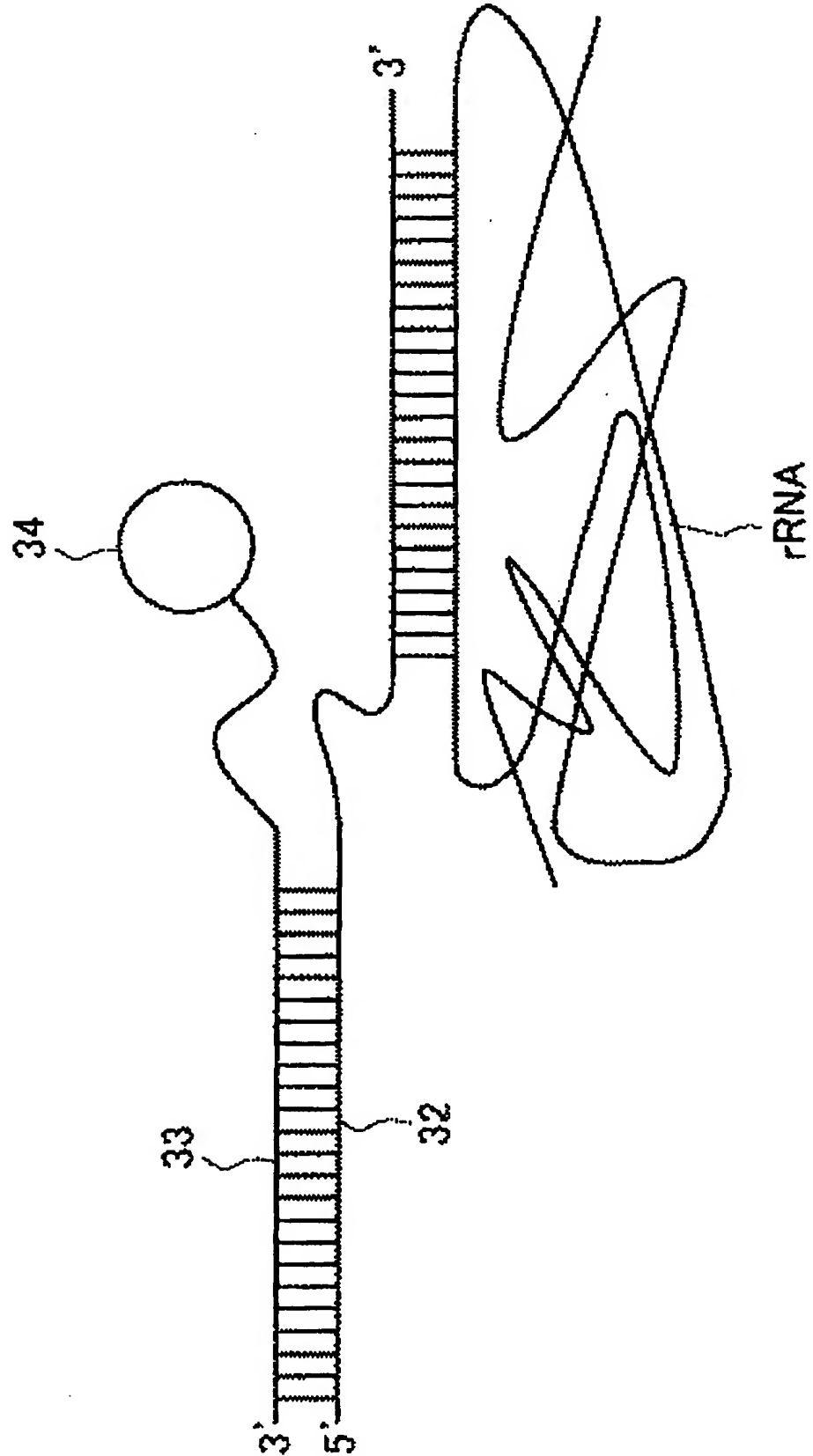


Fig. 4

- (a) 5'-CTCATAGGATCAGATCAGTTGCG-3'
3'-GAGTATCCTAGTCTAGTCAAC-5'
- (b) 5'-GCAATCGCACTTGAACGAT-3'
3'-CGTTAGCGTGAAC TTGCTACTAG-5'

Fig. 5

(a) 5'-CATAGGATCAGATCAGTTGCGCNN-3'

(b) 5'-GCACTAGTGCAATCGCACTTGAACGATGATCNN-3'

Fig. 6

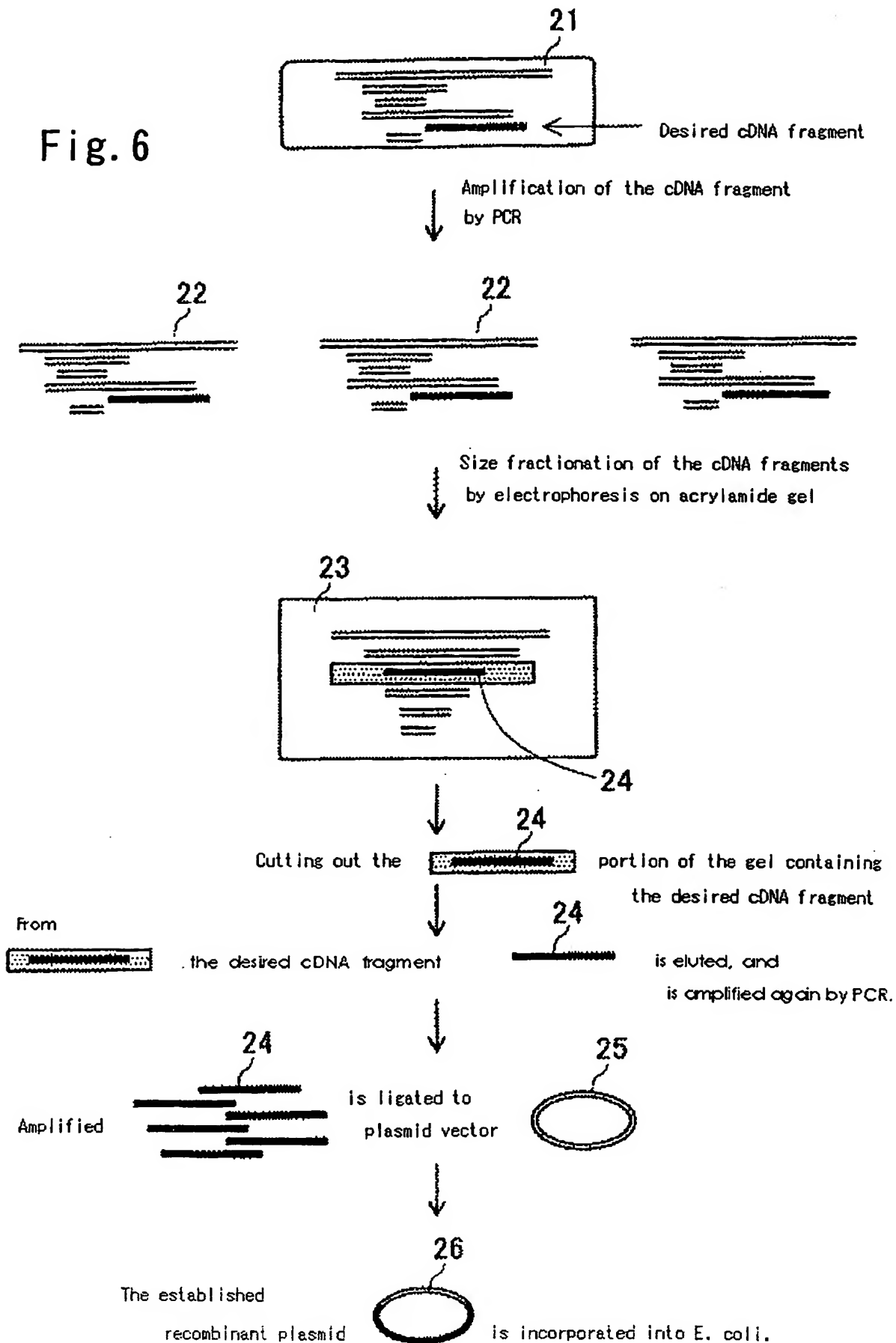


Fig. 7

10 20 30 40 50 60 70 80
ATGAGTATTCAACATTTTCGGTGTGGCCCTTATTCCTTTTGTGGCCATTTTGCCTTCCTGTTTTGCTCACCAGAAAC

90 100 110 120 130 140 150 160
GCTGGTGAAGTAAAAGATGCTGAAGATCACTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAAG
/ Sau3AI / Sau3AI / Sau3AI

170 180 190 200 210 220 230 240
TCCTTGAGAGTTTTTCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCC
/ HhaI

250 260 270 280 290 300 310 320
CGTATTGACGCGGGCAAGAGCAACTCGGTGCGCCGATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCAC

330 340 350 360 370 380 390 400
AGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTCTGCCATAACCATGAGTGATAACACTGCCGCCA

410 420 430 440 450 460 470 480
ACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTTGCAACATGGGGGATCATGTAACTCGCCTT
/ Sau3AI / Sau3AI

490 500 510 520 530 540 550 560
GATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCACGATGCCCTGTAGCAATGGCAACAAC
Sau3AI

570 580 590 600 610 620 630 640
GTTGCGCAAACTATTAACTGGCGAACTACTTACTAGCTTCCCCGCAACAATTAAAGACTGGATGGAGCGCGGATAAAG
/ HhaI

650 660 670 680 690 700 710 720
TTGCAAGGACCACTTCTCGCTCGGCCCTTCCGCTGGCTGCTTATTGCTGATAAATCTGGAGCCGGTGAGCGTCCGCTCT
/ HhaI

730 740 750 760 770 780 790 800
CGCGGTATCATTTGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACGACGGGGAGTCAGGCAAC

810 820 830 840 850 860 870
TATGGATGAACGAAATAGACAGATCGCTGAGATAGGTCCCTCACTGATTAAAGCATTGGTAA
/ Sau3AI

Fig. 8

